

Seq List 1

SEQUENCE LISTING

<110> METZ, JAMES G.
LARDIZABAL, KATHRYN D.
LASSNER, MICHAEL

<120> NUCLEIC ACID SEQUENCES ENCODING A PLANT CYTOPLASMIC
PROTEIN INVOLVED IN FATTY ACYL-COA METABOLISM

<130> 16518.025

<140> 08/657,749

<141> 1996-05-30

<150> PCT/US94/13686

<151> 1994-11-30

<150> 08/265,047

<151> 1994-06-23

<150> 08/160,602

<151> 1993-11-30

<150> 08/066,299

<151> 1993-05-20

<150> PCT/US92/09863

<151> 1992-11-13

<150> 07/933,411

<151> 1992-08-21

<150> 07/796,256

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<170> PatentIn Ver. 2.1

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tat ctt ctt ttg aga gca acc gat gac gag aca gct gct cta cgc ttg 256

Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu

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caa aat gag gtt ttt gga aaa gag ttg ttc aaa gtt ctg aaa caa aat 304

Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn

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tta ggt gca aat ttc tat tcc ttt gta tca gaa aaa gtg act gta gta 352

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Pro Gly Asp Ile Thr Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu

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aca atc aac ttc att gaa agg tac gac gtg tct ctg ctt atc aac aca 496

Thr Ile Asn Phe Ile Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr

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tat gga gcc aag tat gtt ttg gac ttc gcg aag aag tgc aac aaa tta 544

Tyr Gly Ala Lys Tyr Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu

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aga tta ggt ctg gac att aat gta gag aag aaa ctt gtg gag gca aaa Arg Leu Gly Leu Asp Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys	688
190 195 200	
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270 275 280	
atc gat aat gta cct gta tat tat ggt aaa ggg aga ttg agg tgt atg Ile Asp Asn Val Pro Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met	976
285 290 295	
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320 325 330	
gta gag ccg gtg aca tac cat gtg gga tot tca gcg gcg aat cca atg Val Glu Pro Val Thr Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met	1120
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aaa ctg agt gca tta cca gag atg gca cac cgt tac ttc acc aag aat Lys Leu Ser Ala Leu Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn	1168
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 Val Phe Ser Ser Phe Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe
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ctc ctt cct ttg aag gta ctg gag ata gca aat aca ata ttc tgc caa 1312
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tgg ttc aag ggt aag tac atg gat ctt aaa agg aag acg agg ttg ttg 1360
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ttg cgt tta gta gac att tat aaa ccc tac ctc ttc ttc caa ggc atc 1408
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 460 465 470 475

gaa gat tac ttc ttg aaa act cat ttc cca ggn gtc gta gag cac gtt 1552
 Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val
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gtgttgcaagt tttgattcct tgtattgtta cttgtacttt tgatcttttt cttttttaat 1728

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 35 40 45

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Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn Leu Gly Ala Asn Phe
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Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val Pro Gly Asp Ile Thr
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Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu Lys Glu Glu Met Trp
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Arg Glu Ile Asp Val Val Val Asn Leu Ala Ala Thr Ile Asn Phe Ile
115 120 125

Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr Tyr Gly Ala Lys Tyr
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Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu Lys Ile Phe Val His
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Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn Gly Leu Ile Leu Glu
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Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly Arg Leu Gly Leu Asp
180 185 190

Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys Ile Asn Glu Leu Gln
195 200 205

Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser Thr Met Lys Asp Met
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Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro Asn Val Tyr Val Phe
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Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln Tyr Lys Gly Asp Ile
245 250 255

Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr Ser Thr Phe Lys Glu
260 265 270

Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr Ile Asp Asn Val Pro
275 280 285

Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met Leu Cys Gly Pro Ser
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Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val Val Asn Ala Thr Ile
305 310 315 320

Val Ala Met Val Ala His Ala Asn Gln Arg Tyr Val Glu Pro Val Thr
325 330 335

6

Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met Lys Leu Ser Ala Leu
 340 345 350
 Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn Pro Trp Ile Asn Pro
 355 360 365
 Asp Arg Asn Pro Val His Val Gly Arg Ala Met Val Phe Ser Ser Phe
 370 375 380
 Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe Leu Leu Pro Leu Lys
 385 390 395 400
 Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln Trp Phe Lys Gly Lys
 405 410 415
 Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu Leu Arg Leu Val Asp
 420 425 430
 Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile Phe Asp Asp Met Asn
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 Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser Ile Val Glu Ala Asp
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Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr

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act atg acc gcc act ctc ccc aac ttc aag tcc tcc atc aac tta cac 152

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cac gtc aag ctc ggc tac cac tac tta atc tcc aat gcc ctc ttc ctc 200

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gta ttc atc ccc ctt ttg ggc ctc gct tgc gcc cat ctc tcc tcc ttc 248

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tcg gcc cat gac ttg tcc ctg ctc ttc gac ctc ctt cgc cgc aac ctc 296

Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu Arg Arg Asn Leu

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ctc cct gtt gtc gtt tgt tct ttc ctc ttc gtt tta tta gca acc cta 344

Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu Leu Ala Thr Leu

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Tyr Lys Pro Gln Pro Asn Leu Met Thr Ser His Glu Met Phe Met Asp

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Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys
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Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys
505 510 515

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Ile Ala Pro Ile Ala Ser
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 50 55 60
 Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp
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 Val Leu Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr
 100 105 110
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 His Glu Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys
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 Glu Asn Ile Glu Phe Gln Arg Lys Ile Leu Glu Arg Ala Gly Met Gly
 145 150 155 160
 Arg Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Ala Glu Pro
 165 170 175
 Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala
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 Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly
 195 200 205
 Ile Leu Val Val Xaa Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser
 210 215 220
 Ser Met Ile Val Asn His Tyr Lys Xaa Arg Gly Asn Ile Leu Ser Tyr
 225 230 235 240
 Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu
 245 250 255
 Ala Lys Asp Leu Leu Gln Val Tyr Arg Lys Asn Thr Tyr Val Leu Val
 260 265 270
 Val Ser Thr Glu Asn Met Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg
 275 280 285

11

Ser Met Leu Ile Thr Asn Cys Leu Phe Arg Met Gly Gly Ala Ala Ile
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 Ile Leu Ser Asn Arg Trp Arg Asp Arg Arg Arg Ser Lys Tyr Gln Leu
 305 310 315 320
 Leu His Thr Val Arg Thr His Lys Gly Ala Asp Asp Lys Ser Tyr Arg
 325 330 335
 Cys Val Leu Gln Gln Glu Asp Glu Asn Asn Lys Val Gly Val Ala Leu
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 Ser Lys Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys Ala Asn Ile
 355 360 365
 Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu Phe
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 Phe Ala Thr Leu Val Ala Arg Lys Val Phe Lys Met Thr Asn Val Lys
 385 390 395 400
 Pro Tyr Ile Pro Asp Phe Lys Leu Ala Ala Asn Asp Phe Cys Ile His
 405 410 415
 Ala Gly Gly Lys Ala Val Leu Asp Glu Leu Glu Lys Asn Leu Glu Leu
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 Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala
 450 455 460
 Lys Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly
 465 470 475 480
 Ser Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val
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 15 20 25 30

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 Ser Ser Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile
 35 40 45

tcc aat gcc ctc ttc ctc gta ttc atc ccc ctt ttg ggc ctc gct tcg 195
 Ser Asn Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser
 50 55 60

gcc cac ctc tcc tcc ttc tcg gcc cat gac ttg tcc ctg ctc ttc gac 243
 Ala His Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp
 65 70 75

ctc ctt cgc cgc aac ctc ctc ccc gtt gtc gtt tgt tct ttc ctc ttc 291
 Leu Leu Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe
 80 85 90

gtt tta tta gca acc cta cat ttc ttg acc cgg cct agg aat gtc tac 339
 Val Leu Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr
 95 100 105 110

ttg gtg gac ttt gcc tgc tat aag cct cac ccg aac ctg ata aca tcc 387
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 115 120 125

cac gag atg ttc atg gac cgg acc tcc cgg gcc ggg tcg ttt tct aag 435
 His Glu Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys
 130 135 140

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 145 150 155

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 175 180 185 190

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Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly	
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Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser	
210 215 220	
tcc atg ata gtt aac cat tac aag ctt agg ggt aat ata ctt agc tat	723
Ser Met Ile Val Asn His Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr	
225 230 235	
aat ctt ggt ggc atg ggt tgc agt gct ggg ctc att tcc att gat ctt	771
Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu	
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Ala Lys Asp Leu Leu Gln Val Tyr Arg Asn Thr Tyr Val Leu Val Val	
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agc aca gaa aac atg acc ctt aat tgg tac tgg ggc aat gac cgc tcc	867
Ser Thr Glu Asn Met Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser	
275 280 285	
atg ctt atc acc aac tgc cta ttt cgc atg ggt ggc gct gcc atc atc	915
Met Leu Ile Thr Asn Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile	
290 295 300	
ctc tca aac cgc tgg cgt gat cgt cgc cga tcc aag tac caa ctc ctt	963
Leu Ser Asn Arg Trp Arg Asp Arg Arg Arg Ser Lys Tyr Gln Leu Leu	
305 310 315	
cac aca gta cgc acc cac aag ggc gct gac gac aag tcc tat aga tgc	1011
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Val Leu Gln Gln Glu Asp Glu Asn Asn Lys Val Gly Val Ala Leu Ser	
335 340 345 350	
aag gat ctg atg gca gtt gcc ggt gaa gcc cta aag gcc aac atc acg	1107
Lys Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr	
355 360 365	
acc ctt ggt ccc ctc gtg ctc ccc atg tca gaa caa ctc ctc ttc ttt	1155
Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe	
370 375 380	
gcc acc tta gtg gca cgt aag gtc ttc aag atg acg aac gtg aag cca	1203
Ala Thr Leu Val Ala Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro	
385 390 395	

14

tac atc cca gat ttc aag ttg gca gcg aag cac ttc tgc atc cat gca 1251
 Tyr Ile Pro Asp Phe Lys Leu Ala Ala Lys His Phe Cys Ile His Ala
 400 405 410

gga ggc aaa gca gtg ttg gat gag ctc gag acg aac ttg gag ttg acg 1299
 Gly Gly Lys Ala Val Leu Asp Glu Leu Glu Thr Asn Leu Glu Leu Thr
 415 420 425 430

cca tgg cac ctt gaa ccc tcg agg atg aca ctg tat agg ttt ggg aac 1347
 Pro Trp His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn
 435 440 445

aca tcg agt agc tca tta tgg tac gag ttg gca tac gct gaa gca aaa 1395
 Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys
 450 455 460

ggg agg atc cgt aag ggt gat cga act tgg atg att gga ttt ggt tca 1443
 Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser
 465 470 475

ggt ttc aag tgt aac agt gtt gtg tgg agg gct ttg agg agt gtc aat 1491
 Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn
 480 485 490

ccg gct aga gag aag aat cct tgg atg gat gaa att gag aat ttc cct 1539
 Pro Ala Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro
 495 500 505 510

gtc cat gtg cct aaa atc gca cct atc gct tcg tagaactgct aggatgtgat 1592
 Val His Val Pro Lys Ile Ala Pro Ile Ala Ser
 515 520

tagtaatgaa aaatgtgtat tatgttagtg atgtagaaaa agaaacttta gttgatgggt 1652

gagaacatgt ctcattgaga ataacgtgtg catcgttgtg tcgaatttga atttgagtat 1712

tggtgaaatt ctgttagaat tgacgcatga gtcatatata tacaaattta agtaagattt 1772

tacgctttct t 1783

<210> 6

<211> 521

<212> PRT

<213> *Simmondsia chinensis*

<400> 6

Met Lys Ala Lys Thr Ile Thr Asn Pro Glu Ile Gln Val Ser Thr Thr
 1 5 10 15

Met Thr Thr Thr Thr Thr Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser
 20 25 30

15

Ile Asn Leu His His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn
 35 40 45
 Ala Leu Phe Leu Val Phe Ile Pro Leu Leu Gly Leu Ala Ser Ala His
 50 55 60
 Leu Ser Ser Phe Ser Ala His Asp Leu Ser Leu Leu Phe Asp Leu Leu
 65 70 75 80
 Arg Arg Asn Leu Leu Pro Val Val Val Cys Ser Phe Leu Phe Val Leu
 85 90 95
 Leu Ala Thr Leu His Phe Leu Thr Arg Pro Arg Asn Val Tyr Leu Val
 100 105 110
 Asp Phe Ala Cys Tyr Lys Pro His Pro Asn Leu Ile Thr Ser His Glu
 115 120 125
 Met Phe Met Asp Arg Thr Ser Arg Ala Gly Ser Phe Ser Lys Glu Asn
 130 135 140
 Ile Glu Phe Gln Arg Lys Ile Leu Glu Arg Ala Gly Met Gly Arg Glu
 145 150 155 160
 Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Pro Glu Pro Ser Ile
 165 170 175
 Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp
 180 185 190
 Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly Ile Leu
 195 200 205
 Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ser Met
 210 215 220
 Ile Val Asn His Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Leu
 225 230 235 240
 Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu Ala Lys
 245 250 255
 Asp Leu Leu Gln Val Tyr Arg Asn Thr Tyr Val Leu Val Val Ser Thr
 260 265 270
 Glu Asn Met Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser Met Leu
 275 280 285
 Ile Thr Asn Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile Leu Ser
 290 295 300
 Asn Arg Trp Arg Asp Arg Arg Arg Ser Lys Tyr Gln Leu Leu His Thr
 305 310 315 320

16

Val Arg Thr His Lys Gly Ala Asp Asp Lys Ser Tyr Arg Cys Val Leu
 325 330 335

Gln Gln Glu Asp Glu Asn Asn Lys Val Gly Val Ala Leu Ser Lys Asp
 340 345 350

Leu Met Ala Val Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Leu
 355 360 365

Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe Ala Thr
 370 375 380

Leu Val Ala Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro Tyr Ile
 385 390 395 400

Pro Asp Phe Lys Leu Ala Ala Lys His Phe Cys Ile His Ala Gly Gly
 405 410 415

Lys Ala Val Leu Asp Glu Leu Glu Thr Asn Leu Glu Leu Thr Pro Trp
 420 425 430

His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn Thr Ser
 435 440 445

Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys Gly Arg
 450 455 460

Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe
 465 470 475 480

Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala
 485 490 495

Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro Val His
 500 505 510

Val Pro Lys Ile Ala Pro Ile Ala Ser
 515 520

<210> 7

<211> 1647

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oleosin
 expression cassette

<400> 7

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 aacatcgagc aagctctcaa agctgacctc ttctggatcg tactgaaccc gaacaatctc 120
 gttatgtccc gtcgtctccg aacagacatc ctctagctc ggattatcga cgaatccatg 180

17

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gctataccca accctccgtct tcgtcacgcc tggaaacctc tggtagacca attccgctcc 240
ccagaagcaa ccggcgcgga attgcgcgaa ttgctgacct ggagacggaa catcgtcgtc 300
gggtcccttg cgcattgcgg cggaagccgg gtcgggttgg ggacgagacc cgaatccgag 360
cctgggtgaag aggttggttca tcggagattt atagacggag atggatcgag cgggttttggg 420
gaaaggggaa gtgggttttg ctcttttggg tagagagagt gcagcttttg agagagactg 480
gagagggtta gagagagacg cggcggatat taccggagga gaggcgacga gagatagcat 540
tatcgaaggg gagggagaaa gagtgcgtg gagaaataag aaaccgttaa ggtcgggata 600
tttatcatat taaaagccca atgggcctga acccatttaa acaagacaga taaatgggccc 660
gtgtgttaag ttaacagagt gttaacgttc ggtttcaaat gccaacgcca taggaacaaa 720
acaaacgtgt cctcaagtaa acccctgccg ttacacctc aatggctgca tgggtgaagcc 780
attaacacgt ggcgtaggat gcatgacgac gccattgaca cctgactctc ttcccttctc 840
ttcatataat tctaataaat tcaactactc attgtcatag ctattcggaa aatacataca 900
catccttttc tcttcgatct ctctcaatc acaagaagca aagtcgacgg atccctgcag 960
taaattacgc catgactatt ttcatagtcc aataaggctg atgtcgggag tccagtttat 1020
gagcaataag gtgttttaga tttgatcaat gtttataata aaagggggaa gatgatata 1080
cagtcttttg ttcttttttg cttttgttaa atttgtgtgt ttctatttgt aaacctcctg 1140
tatatgttgt acttctttcc ctttttaagt ggtatcgtct atatggtaaa acgttatgtt 1200
tggtctttcc tttctctgtt ttaggataaa aagactgcat gttttatctt tagttatatt 1260
atgttgagta aatgaacttt catagatctg gttccgtaga gtagactagc agccgagctg 1320
agetgaactg aacagctggc aatgtgaaca ctggatgcaa gatcagatgt gaagatctct 1380
aatatgggtg tgggattgaa catatcgtgt ctatatctt gttggcatta agctcttaac 1440
atagatataa ctgatgcagt cattgggtca tacacatata tagtaaggaa ttacaatggc 1500
aaccctaac tcaaaaacag taggccacct gaattgcctt atcgaataag agtttgtttc 1560
cccccactc atgggatgta atacatggga tttgggagtt tgaatgaacg ttgagacatg 1620
gcagaacctc tagaggtacc ggccgcgc 1647

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<210> 8

<211> 1810

<212> DNA

<213> Brassica sp.

<220>

<221> CDS

<222> (4)..(1647)

<400> 8

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gaa atg agt agg tct agc gaa caa gat cta ctc tct acc gag att gtt 48
Met Ser Arg Ser Ser Glu Gln Asp Leu Leu Ser Thr Glu Ile Val
1 5 10 15

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aac cgt ggg atc gaa cct tcc ggt cca aac gcc ggt tca cca acg ttc 96
Asn Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe
20 25 30

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tcg gtc aga gtc cgg aga cgt tta ccg gat ttt ctt caa tcc gta aac 144
Ser Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn
35 40 45

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ttg aag tac gtg aaa ctt ggt tat cac tac ctc ata aac cat gcg gtt 192
Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val
50 55 60

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18

tac ttg gcg acg ata ccg gtt ctt gtg ctt gtg ttt agt gcc gaa gtt	240
Tyr Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val	
65 70 75	
ggg agt tta agc gga gaa gag att tgg aag aag ctt tgg gac tat gat	288
Gly Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp	
80 85 90 95	
atc gca acc gtc atc gga ttc ttc ggt gtc ttt gtc ttg acc gtt tgc	336
Ile Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys	
100 105 110	
gtc tac ttc atg tet cgt cca cga tct gtt tat ctc att gac ttc gct	384
Val Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala	
115 120 125	
tgt ttc aag cct tcc gat gaa ctt aag gtg aca aga gaa gag ttc ata	432
Cys Phe Lys Pro Ser Asp Glu Leu Lys Val Thr Arg Glu Glu Phe Ile	
130 135 140	
gat cta gct aga aaa tca ggc aag ttc gac gaa gag atc ctc gga ttc	480
Asp Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Ile Leu Gly Phe	
145 150 155	
aag aag agg atc ctt caa gcc tca gga ata ggc gat gaa acg tac gtc	528
Lys Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val	
160 165 170 175	
cca aga tca atc tct tcg tcg gaa aac aca aca acg atg aaa gaa ggt	576
Pro Arg Ser Ile Ser Ser Ser Glu Asn Thr Thr Thr Met Lys Glu Gly	
180 185 190	
cgt gaa gaa gcc tcg atg atg ata ttc ggc gca ctc gac gaa ctc ttc	624
Arg Glu Glu Ala Ser Met Met Ile Phe Gly Ala Leu Asp Glu Leu Phe	
195 200 205	
gag aag aca cgt gtc aaa ccg aaa gac gta ggt gtc ctc gtg gtt aac	672
Glu Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn	
210 215 220	
tgc agt atc ttt aac ccg act ccg tca ctc tcc gcg atg gtg att aac	720
Cys Ser Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn	
225 230 235	
cac tac aag atg aga ggg aac ata ctt agc tac aac cta gga ggg atg	768
His Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met	
240 245 250 255	
ggt tgc tca gca gga atc ata gcc gtt gat ctt gct cgt gac atg ctt	816
Gly Cys Ser Ala Gly Ile Ile Ala Val Asp Leu Ala Arg Asp Met Leu	
260 265 270	

19

cag tct aac ccg aat agt tac gcg gtg gtt gtg agt acc gag atg gtt Gln Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val	864
275 280 285	
ggg tat aat tgg tac gtg gga cgt gac aag tca atg gtt ata cct aac Gly Tyr Asn Trp Tyr Val Gly Arg Asp Lys Ser Met Val Ile Pro Asn	912
290 295 300	
tgc ttc ttt agg atg ggt tgc tcc gcc gtt atg ctg tct aac cgc cgc Cys Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg	960
305 310 315	
cgt gac ttc cgc cat gct aag tac cgc ctt gag cac att gtc cgg act Arg Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr	1008
320 325 330 335	
cac aag gct gcc gac gac cgt agc ttc agg agt gtg tac cag gaa gaa His Lys Ala Ala Asp Asp Arg Ser Phe Arg Ser Val Tyr Gln Glu Glu	1056
340 345 350	
gat gaa caa gga ttc aag gga tta aaa ata agc aga gac cta atg gaa Asp Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu	1104
355 360 365	
gtt gga ggt gaa gct ctc aag acc aac atc acc acc tta ggc cct ctc Val Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu	1152
370 375 380	
gtc ott cct ttc tcc gag cag ctt ctc ttc ttt gcc got ttg atc cgt Val Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Ile Arg	1200
385 390 395	
aga act ttc tca ccc gcc gcc aaa act acc acc acc tcc tcc tca gcc Arg Thr Phe Ser Pro Ala Ala Lys Thr Thr Thr Ser Ser Ser Ala	1248
400 405 410 415	
act gcg aaa atc aac gga gcc aag tcg tca tcc tcc tct gat cta tcc Thr Ala Lys Ile Asn Gly Ala Lys Ser Ser Ser Ser Ser Asp Leu Ser	1296
420 425 430	
aag ccg tac atc ccg gac tac aag ctt gcc ttc gag cat ttc tgc ttc Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys Phe	1344
435 440 445	
cac gcg gca agc aaa gcg gtg ctt gag gag ctt cag aag aat cta ggc His Ala Ala Ser Lys Ala Val Leu Glu Glu Leu Gln Lys Asn Leu Gly	1392
450 455 460	
ttg agt gat gag aac atg gag gct tot aag atg act tta cac agg ttt Leu Ser Asp Glu Asn Met Glu Ala Ser Lys Met Thr Leu His Arg Phe	1440
465 470 475	

20

gga aac act tcc agc agt gga atc tgg tac gag ctt gct tac atg gag 1488
 Gly Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met Glu
 480 485 490 495

gcc aag gag agt gtt cgt aga ggc gat agg gtt tgg cag att gct ttt 1536
 Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala Phe
 500 505 510

ggg tca ggt ttt aag tgt aac agt gtg gtt tgg aag gca atg agg aag 1584
 Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg Lys
 515 520 525

gtg aag aag ccg gca agg aac aat cct tgg gtt gat tgc att aac cgt 1632
 Val Lys Lys Pro Ala Arg Asn Asn Pro Trp Val Asp Cys Ile Asn Arg
 530 535 540

tac cct gtc gct ctc tgatcattta tttttaaaat tattatttct tottaattaa 1687
 Tyr Pro Val Ala Leu
 545

atcatctatg atctctcttc cttgttggtg gatgatagac gtttggttgc tggtcattcg 1747

tatcttaaga ctcttataag aatggatggt tcaagtccaa aaaaaaaaaa aaaaaaaaaa 1807

aaa 1810

<210> 9

<211> 548

<212> PRT

<213> Brassica sp.

<400> 9

Met Ser Arg Ser Ser Glu Gln Asp Leu Leu Ser Thr Glu Ile Val Asn
 1 5 10 15

Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe Ser
 20 25 30

Val Arg Val Arg Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn Leu
 35 40 45

Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val Tyr
 50 55 60

Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val Gly
 65 70 75 80

Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp Ile
 85 90 95

Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys Val
 100 105 110

21

Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala Cys
 115 120 125
 Phe Lys Pro Ser Asp Glu Leu Lys Val Thr Arg Glu Glu Phe Ile Asp
 130 135 140
 Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Ile Leu Gly Phe Lys
 145 150 155 160
 Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val Pro
 165 170 175
 Arg Ser Ile Ser Ser Ser Glu Asn Thr Thr Thr Met Lys Glu Gly Arg
 180 185 190
 Glu Glu Ala Ser Met Met Ile Phe Gly Ala Leu Asp Glu Leu Phe Glu
 195 200 205
 Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn Cys
 210 215 220
 Ser Ile Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Ile Asn His
 225 230 235 240
 Tyr Lys Met Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly
 245 250 255
 Cys Ser Ala Gly Ile Ile Ala Val Asp Leu Ala Arg Asp Met Leu Gln
 260 265 270
 Ser Asn Pro Asn Ser Tyr Ala Val Val Val Ser Thr Glu Met Val Gly
 275 280 285
 Tyr Asn Trp Tyr Val Gly Arg Asp Lys Ser Met Val Ile Pro Asn Cys
 290 295 300
 Phe Phe Arg Met Gly Cys Ser Ala Val Met Leu Ser Asn Arg Arg Arg
 305 310 315 320
 Asp Phe Arg His Ala Lys Tyr Arg Leu Glu His Ile Val Arg Thr His
 325 330 335
 Lys Ala Ala Asp Asp Arg Ser Phe Arg Ser Val Tyr Gln Glu Glu Asp
 340 345 350
 Glu Gln Gly Phe Lys Gly Leu Lys Ile Ser Arg Asp Leu Met Glu Val
 355 360 365
 Gly Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val
 370 375 380
 Leu Pro Phe Ser Glu Gln Leu Leu Phe Phe Ala Ala Leu Ile Arg Arg
 385 390 395 400

22

Thr Phe Ser Pro Ala Ala Lys Thr Thr Thr Thr Ser Ser Ser Ala Thr
405 410 415

Ala Lys Ile Asn Gly Ala Lys Ser Ser Ser Ser Ser Asp Leu Ser Lys
420 425 430

Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys Phe His
435 440 445

Ala Ala Ser Lys Ala Val Leu Glu Glu Leu Gln Lys Asn Leu Gly Leu
450 455 460

Ser Asp Glu Asn Met Glu Ala Ser Lys Met Thr Leu His Arg Phe Gly
465 470 475 480

Asn Thr Ser Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met Glu Ala
485 490 495

Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala Phe Gly
500 505 510

Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg Lys Val
515 520 525

Lys Lys Pro Ala Arg Asn Asn Pro Trp Val Asp Cys Ile Asn Arg Tyr
530 535 540

Pro Val Ala Leu
545

<210> 10

<211> 1442

<212> DNA

<213> Brassica sp.

<220>

<221> CDS

<222> (10) .. (1434)

<400> 10

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Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile
1 5 10

acc aac ctt ttc aac ctt tgt ttc ttt cca tta acg gcg atc gtc gcc 99
Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala
15 20 25 30

gga aaa gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat 147
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr
35 40 45

23

tcc tat ctc caa cac aac ctc ata acc att gct cca ctc ttt gcc ttc	195
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe	
50 55 60	
acc gtt ttc ggt tgg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt	243
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val	
65 70 75	
tac ctc gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca	291
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser	
80 85 90	
agt atc tcc aag gtc atg gat atc ttt tac caa gta aga aaa gct gat	339
Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp	
95 100 105 110	
cct tct cgg aac ggc acg tgc gat gac tgg tcc tgg ctt gac ttc ttg	387
Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu	
115 120 125	
agg aag att caa gaa cgt tca ggt cta ggc gat gaa acc cac ggg ccc	435
Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro	
130 135 140	
gag ggg ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt	483
Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg	
145 150 155	
gaa gag acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag	531
Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys	
160 165 170	
aac acc aat gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca	579
Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser	
175 180 185 190	
agc atg ttt aat cca act cct tgg ctc tcc gcg atg gtc gtt aac act	627
Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr	
195 200 205	
ttc aag ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt	675
Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly	
210 215 220	
tgt agt gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat	723
Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His	
225 230 235	
gtc cat aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act	771
Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr	
240 245 250	

24

tat aac att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc	819
Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys	
255 260 265 270	
ttg ttc cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct aga	867
Leu Phe Arg Val Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg	
275 280 285	
gat cgt aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat	915
Asp Arg Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His	
290 295 300	
acc gga gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gtt	963
Thr Gly Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Val	
305 310 315	
gag aac ggc aaa acc gga gtg agt ttg tcc aag gac ata acc gat gtt	1011
Glu Asn Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val	
320 325 330	
gct ggt cga acg gtt aag aaa aac ata gca acg ctg ggt ccg ttg att	1059
Ala Gly Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile	
335 340 345 350	
ctt ccg tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag	1107
Leu Pro Leu Ser Gly Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys	
355 360 365	
aaa ctt ttc aaa gac aaa atc aaa cat tat tac gtc ccg gac ttc aag	1155
Lys Leu Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys	
370 375 380	
ctt gct atc gac cat ttt tgt ata cat gcc gga ggc aaa gcc gtg att	1203
Leu Ala Ile Asp His Phe Cys Ile His Ala Gly Gly Lys Ala Val Ile	
385 390 395	
gat gtg cta gag aag aac cta ggc cta gca ccg atc gat gta gag gca	1251
Asp Val Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala	
400 405 410	
tca aga tca acg tta cat aga ttt gga aac act tca tct agc tca ata	1299
Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile	
415 420 425 430	
tgg tat gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt	1347
Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly	
435 440 445	
aat aaa gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt	1395
Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser	
450 455 460	

25

gca gtt tgg gtg gct cta aac aat gtc aaa gct tcc aaa taggatcc 1442
 Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys
 465 470 475

<210> 11
 <211> 475
 <212> PRT
 <213> Brassica sp.

<400> 11
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 1 5 10 15
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220

26

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Val Glu Asn
 305 310 315 320
 Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Lys Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys
 465 470 475

<210> 12

<211> 1442

<212> DNA

<213> Brassica sp.

27

<220>

<221> CDS

<222> (10) .. (1434)

<400> 12

gtcgacaaa atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata 51

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile

1

5

10

acc aac ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc 99

Thr Asn Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala

15

20

25

30

gga aaa gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat 147

Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr

35

40

45

tcc tat ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc 195

Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe

50

55

60

acc gtt ttc ggt tcc gtt ctc tac atc gca acc cgg ccc aaa ccg gtt 243

Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val

65

70

75

tac ctc gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca 291

Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser

80

85

90

agt atc tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat 339

Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp

95

100

105

110

cct tct cgg aac ggc acg tgc gat gac tcc tcc tgg ctt gac ttc ttg 387

Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu

115

120

125

agg aag att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc 435

Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro

130

135

140

gag ggg ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt 483

Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg

145

150

155

gaa gag acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag 531

Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys

160

165

170

aac acc aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca 579

Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser

175

180

185

190

28

agc atg ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act	627
Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr	
195 200 205	
ttc aag ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt	675
Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly	
210 215 220	
tgt agt gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat	723
Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His	
225 230 235	
gtc cat aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act	771
Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr	
240 245 250	
tat aac att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc	819
Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys	
255 260 265 270	
ttg ttc cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga	867
Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly	
275 280 285	
gat cgt aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat	915
Asp Arg Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His	
290 295 300	
acc gga gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat	963
Thr Gly Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp	
305 310 315	
gag aac ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt	1011
Glu Asn Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val	
320 325 330	
gct ggt cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att	1059
Ala Gly Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile	
335 340 345 350	
ctt ccg tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag	1107
Leu Pro Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys	
355 360 365	
aaa ctt ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa	1155
Lys Leu Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys	
370 375 380	
ctt gct att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att	1203
Leu Ala Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile	
385 390 395	

29

gat gtg cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca 1251
 Asp Val Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala
 400 405 410

tca aga tca acg tta cat aga ttt gga aac act tca tct agc tca ata 1299
 Ser Arg Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile
 415 420 425 430

tgg tat gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt 1347
 Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly
 435 440 445

aat aaa gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt 1395
 Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser
 450 455 460

gca gtt tgg gtg gct cta aac aat gtc aaa gct tcc aaa taggatcc 1442
 Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys
 465 470 475

<210> 13

<211> 475

<212> PRT

<213> Brassica sp.

<400> 13

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15

Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30

Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45

Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60

Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80

Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95

Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
 100 105 110

Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

30

Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
 245 250 255
 Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

31

Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435 440 445

Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450 455 460

Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys
465 470 475

<210> 14

<211> 623

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(623)

<400> 14

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aag ctt aaa cta gtg tat cat tac cta atc tcc aac gct ctc tac atc      48
Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Leu Tyr Ile
  1              5              10              15

ctc ctc ctt cct ctc ctc gcc gca aca atc gct aac ctc tct tct ttc      96
Leu Leu Leu Pro Leu Leu Ala Ala Thr Ile Ala Asn Leu Ser Ser Phe
          20              25              30

acc atc aac gac ctc tct ctc ctc tac aac aca ctc cgt ttc cat ttc      144
Thr Ile Asn Asp Leu Ser Leu Leu Tyr Asn Thr Leu Arg Phe His Phe
          35              40              45

ctc tcc gcc aca ctc gcc acc gca ctc ttg atc tct ctc tcc acc gct      192
Leu Ser Ala Thr Leu Ala Thr Ala Leu Leu Ile Ser Leu Ser Thr Ala
          50              55              60

tac ttc acc acc cgt cct cgc cgt gtc ttc ctc ctc gac ttc tcg tgt      240
Tyr Phe Thr Thr Arg Pro Arg Arg Val Phe Leu Leu Asp Phe Ser Cys
          65              70              75              80

tac aaa cca gac cct tca ctg atc tgc act cgt gaa aca ttc atg gac      288
Tyr Lys Pro Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp
          85              90              95

aga tct caa cgt gta ggc atc ttc aca gaa gac aac tta gct ttc caa      336
Arg Ser Gln Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln
          100              105              110

caa aag atc ctc gaa aga tcc ggt cta ggt cag aaa act tac ttc cct      384
Gln Lys Ile Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro
          115              120              125

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32

gaa gct ctt ctt cgt gtt cct cct aat cct tgt atg gaa gaa gcg aga 432
 Glu Ala Leu Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg
 130 135 140

aaa gag gca gaa aca gtt atg ttc gga gct att gac gcg gtt ctt gag 480
 Lys Glu Ala Glu Thr Val Met Phe Gly Ala Ile Asp Ala Val Leu Glu
 145 150 155 160

aag acc ggt gtg aaa cct aaa gat att gga atc ctt gtg gtg aat tgt 528
 Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
 165 170 175

agc ttg ttt aat cca aca ccg tca ctt tct gct atg att gtg aat aag 576
 Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
 180 185 190

tat aag ctt aga ggc aac att ttg agc tat aat ttc ggc ggg atg gg 623
 Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Phe Gly Gly Met Gly
 195 200 205

<210> 15

<211> 208

<212> PRT

<213> Arabidopsis thaliana

<400> 15

Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Leu Tyr Ile
 1 5 10 15

Leu Leu Leu Pro Leu Leu Ala Ala Thr Ile Ala Asn Leu Ser Ser Phe
 20 25 30

Thr Ile Asn Asp Leu Ser Leu Leu Tyr Asn Thr Leu Arg Phe His Phe
 35 40 45

Leu Ser Ala Thr Leu Ala Thr Ala Leu Leu Ile Ser Leu Ser Thr Ala
 50 55 60

Tyr Phe Thr Thr Arg Pro Arg Arg Val Phe Leu Leu Asp Phe Ser Cys
 65 70 75 80

Tyr Lys Pro Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp
 85 90 95

Arg Ser Gln Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln
 100 105 110

Gln Lys Ile Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro
 115 120 125

Glu Ala Leu Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg
 130 135 140

33

Lys Glu Ala Glu Thr Val Met Phe Gly Ala Ile Asp Ala Val Leu Glu
145 150 155 160

Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
165 170 175

Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
180 185 190

Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Phe Gly Gly Met Gly
195 200 205

<210> 16

<211> 607

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(606)

<400> 16

aag ctt aag tta ggc tac cac tat ctg atc act cac ttt ttt aaa ctc 48
Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Phe Phe Lys Leu
1 5 10 15

atg ttc ctc cct cta atg gct gtt ttg ttc atg aat gtc tca ttg tta 96
Met Phe Leu Pro Leu Met Ala Val Leu Phe Met Asn Val Ser Leu Leu
20 25 30

agc cta aac cat ctt cag ctc tat tac aat tcc acc gga ttc atc ttc 144
Ser Leu Asn His Leu Gln Leu Tyr Tyr Asn Ser Thr Gly Phe Ile Phe
35 40 45

gtc atc act ctc gcc att gtc gga tcc att gtc ttc ttc atg tct cga 192
Val Ile Thr Leu Ala Ile Val Gly Ser Ile Val Phe Phe Met Ser Arg
50 55 60

cct aga tcc atc tac ctt cta gat tac tct tgc tac ctc ccg cct tcg 240
Pro Arg Ser Ile Tyr Leu Leu Asp Tyr Ser Cys Tyr Leu Pro Pro Ser
65 70 75 80

agt caa aaa gtt agc tac cag aaa ttc atg aac aac tct agt ttg att 288
Ser Gln Lys Val Ser Tyr Gln Lys Phe Met Asn Asn Ser Ser Leu Ile
85 90 95

caa gat ttc agc gaa act tct ctt gag ttc cag agg aag atc ttg att 336
Gln Asp Phe Ser Glu Thr Ser Leu Glu Phe Gln Arg Lys Ile Leu Ile
100 105 110

34

cgc tct ggt ctc ggt gaa gag act tat tta ccg gat tct att cac tct 384
 Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Asp Ser Ile His Ser
 115 120 125

atc cct ccg cgt cct act atg gct gca gcg cgt gaa gaa gcg gag cag 432
 Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ala Glu Gln
 130 135 140

gta atc ttc ggt gca ctc gac aat ctt ttc gag aat aca aaa atc aat 480
 Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys Ile Asn
 145 150 155 160

cct agg gag att ggt gtt ctt gtt gtg aat tgt agt ttg ttt aac ccc 528
 Pro Arg Glu Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn Pro
 165 170 175

acg cct tct tta tcc gcc atg att gtt aac aag tat aag ctt aga gga 576
 Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly
 180 185 190

aac att aag agc ttt aat ctc ggc ggc atg g 607
 Asn Ile Lys Ser Phe Asn Leu Gly Gly Met
 195 200

<210> 17

<211> 202

<212> PRT

<213> Arabidopsis thaliana

<400> 17

Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Phe Phe Lys Leu
 1 5 10 15

Met Phe Leu Pro Leu Met Ala Val Leu Phe Met Asn Val Ser Leu Leu
 20 25 30

Ser Leu Asn His Leu Gln Leu Tyr Tyr Asn Ser Thr Gly Phe Ile Phe
 35 40 45

Val Ile Thr Leu Ala Ile Val Gly Ser Ile Val Phe Phe Met Ser Arg
 50 55 60

Pro Arg Ser Ile Tyr Leu Leu Asp Tyr Ser Cys Tyr Leu Pro Pro Ser
 65 70 75 80

Ser Gln Lys Val Ser Tyr Gln Lys Phe Met Asn Asn Ser Ser Leu Ile
 85 90 95

Gln Asp Phe Ser Glu Thr Ser Leu Glu Phe Gln Arg Lys Ile Leu Ile
 100 105 110

Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Asp Ser Ile His Ser
 115 120 125

35

Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ala Glu Gln
 130 135 140

Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys Ile Asn
 145 150 155 160

Pro Arg Glu Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn Pro
 165 170 175

Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly
 180 185 190

Asn Ile Lys Ser Phe Asn Leu Gly Gly Met
 195 200

<210> 18
 <211> 622
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1) .. (621)

<400> 18

aag ctt aaa ctg ggg tac cac tac ctc att act cat ctc ttc aag ctc	48
Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Leu Phe Lys Leu	
1 5 10 15	
tgt ttg gtt cca tta atg gcg gtt tta gtc aca gag atc tcc cga tta	96
Cys Leu Val Pro Leu Met Ala Val Leu Val Thr Glu Ile Ser Arg Leu	
20 25 30	
aca aca gac gat ctt tac cag att tgc ctt cat ctc caa tac aat ctc	144
Thr Thr Asp Asp Leu Tyr Gln Ile Cys Leu His Leu Gln Tyr Asn Leu	
35 40 45	
gtt gct ttc atc ttt ctc tct gct tta gct atc ttt ggc tcc acc gtt	192
Val Ala Phe Ile Phe Leu Ser Ala Leu Ala Ile Phe Gly Ser Thr Val	
50 55 60	
tac atc atg agt cgt ccc aga tct gtt tat ctc gtt gat tac tct tgt	240
Tyr Ile Met Ser Arg Pro Arg Ser Val Tyr Leu Val Asp Tyr Ser Cys	
65 70 75 80	
tat ctt cct ccg gag agt ctt cag gtt aag tat cag aag ttt atg gat	288
Tyr Leu Pro Pro Glu Ser Leu Gln Val Lys Tyr Gln Lys Phe Met Asp	
85 90 95	

36

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cat tct aag ttg att gaa gat ttc aat gag tca tct tta gag ttt cag 336
His Ser Lys Leu Ile Glu Asp Phe Asn Glu Ser Ser Leu Glu Phe Gln
      100                      105                      110

agg aag att ctt gaa cgt tct ggt tta gga gaa gag act tat ctc cct 384
Arg Lys Ile Leu Glu Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro
      115                      120                      125

gaa gct tta cat tgt atc cct ccg agg cct acg atg atg gcg gct cgt 432
Glu Ala Leu His Cys Ile Pro Pro Arg Pro Thr Met Met Ala Ala Arg
      130                      135                      140

gag gaa gct gag cag gta atg ttt ggt gct ctt gat aag ctt ttc gag 480
Glu Glu Ala Glu Gln Val Met Phe Gly Ala Leu Asp Lys Leu Phe Glu
      145                      150                      155                      160

aat acc aag att aac cct agg gat att ggt gtg ttg gtt gtg aat tgt 528
Asn Thr Lys Ile Asn Pro Arg Asp Ile Gly Val Leu Val Val Asn Cys
      165                      170                      175

agc ttg ttt aat cct aca cct tcg ttg tca gct atg att gtt aac aag 576
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
      180                      185                      190

tat aag ctt aga ggg aat gtt aag agt ttt aac ctg ggg ggc att g 622
Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Ile
      195                      200                      205

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<210> 19

<211> 207

<212> PRT

<213> Arabidopsis thaliana

<400> 19

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Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Leu Phe Lys Leu
  1                      5                      10                      15

Cys Leu Val Pro Leu Met Ala Val Leu Val Thr Glu Ile Ser Arg Leu
      20                      25                      30

Thr Thr Asp Asp Leu Tyr Gln Ile Cys Leu His Leu Gln Tyr Asn Leu
      35                      40                      45

Val Ala Phe Ile Phe Leu Ser Ala Leu Ala Ile Phe Gly Ser Thr Val
      50                      55                      60

Tyr Ile Met Ser Arg Pro Arg Ser Val Tyr Leu Val Asp Tyr Ser Cys
      65                      70                      75                      80

Tyr Leu Pro Pro Glu Ser Leu Gln Val Lys Tyr Gln Lys Phe Met Asp
      85                      90                      95

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37

His Ser Lys Leu Ile Glu Asp Phe Asn Glu Ser Ser Leu Glu Phe Gln
 100 105 110

Arg Lys Ile Leu Glu Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro
 115 120 125

Glu Ala Leu His Cys Ile Pro Pro Arg Pro Thr Met Met Ala Ala Arg
 130 135 140

Glu Glu Ala Glu Gln Val Met Phe Gly Ala Leu Asp Lys Leu Phe Glu
 145 150 155 160

Asn Thr Lys Ile Asn Pro Arg Asp Ile Gly Val Leu Val Val Asn Cys
 165 170 175

Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys
 180 185 190

Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Ile
 195 200 205

<210> 20
 <211> 625
 <212> DNA
 <213> Lunaria annua

<220>
 <221> CDS
 <222> (1)..(624)

<400> 20
 aag ctt aag tta tgg tat cac tac ctg att tct cac ctt ttt aag ctc 48
 Lys Leu Lys Leu Trp Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu
 1 5 10 15

ttg ttg gtt cct tta atg gcg gtt ctg ttc acg aat gtc tcc cgg tta 96
 Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu
 20 25 30

agc cta aac cag ctc tgt ctc gat ctc tct ctc cag ctc cag ttc aat 144
 Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn
 35 40 45

ctc gtc gga ttc atc ttc ttc att acc gtc tcc att ttc gga ttc aca 192
 Leu Val Gly Phe Ile Phe Phe Ile Thr Val Ser Ile Phe Gly Phe Thr
 50 55 60

gtt atc ttc atg tcc cga cct aga tcc gtt tac ctc ctc gac tac tca 240
 Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser
 65 70 75 80

38

tgt tac ctc ccg ccg tcg aat ctc aaa gtt agc tac cag aca ttc atg 288
 Cys Tyr Leu Pro Pro Ser Asn Leu Lys Val Ser Tyr Gln Thr Phe Met
 85 90 95

aat cat tct aaa ctg att gaa gat ttc gac gag tcg tcg ctt gag ttc 336
 Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe
 100 105 110

cag cgg aag atc ctg aag cga tcc ggt ctc ggc gaa gag act tac ctc 384
 Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu
 115 120 125

ccg gaa tct atc cac tgc atc ccg ccg cgt ccg act atg gcg gcg gcg 432
 Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala
 130 135 140

cgt gag gaa tcg gag cag gta atc ttc ggt gca ctc gac aat ctc ttc 480
 Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe
 145 150 155 160

gag aat acc aaa atc gac cct agg gag att ggt gtt gtg gtg gtg aac 528
 Glu Asn Thr Lys Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn
 165 170 175

tgc agc ttg ttt aac ccg acg cct tct tta tcc gcc atg att gtg aac 576
 Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn
 180 185 190

aag tat aag ctt aga gga aac gtg aag agc ttt aat ctc ggt ggc atg g 625
 Lys Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met
 195 200 205

<210> 21

<211> 208

<212> PRT

<213> Lunaria annua

<400> 21

Lys Leu Lys Leu Trp Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu
 1 5 10 15

Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu
 20 25 30

Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn
 35 40 45

Leu Val Gly Phe Ile Phe Phe Ile Thr Val Ser Ile Phe Gly Phe Thr
 50 55 60

Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser
 65 70 75 80

39

Cys Tyr Leu Pro Pro Ser Asn Leu Lys Val Ser Tyr Gln Thr Phe Met
85 90 95

Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe
100 105 110

Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu
115 120 125

Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala
130 135 140

Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe
145 150 155 160

Glu Asn Thr Lys Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn
165 170 175

Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn
180 185 190

Lys Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met
195 200 205

<210> 22

<211> 1704

<212> DNA

<213> Lunaria annua

<220>

<221> CDS

<222> (42)..(1535)

<220>

<221> modified_base

<222> (345)

<223> a, c, t, or g

<400> 22

gttcattgat ttgtttgaga ctctgttgca gaaatctcca c atg gat gat gaa tcc 56
Met Asp Asp Glu Ser
1 5

gtt aat gga gga tcc gta cag atc cgg acc cga aag tac gtc aag ctg 104
Val Asn Gly Gly Ser Val Gln Ile Arg Thr Arg Lys Tyr Val Lys Leu
10 15 20

ggc tat cac tac ctg att tct cac ctt ttt aag ctc ttg ttg gtt cct 152
Gly Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu Leu Leu Val Pro
25 30 35

40

tta atg gcg gtt ctg ttc acg aat gtc tcc cgg tta agc cta aac cag	200
Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu Ser Leu Asn Gln	
40 45 50	
ctc tgt ctc gat ctc tct ctc cag ctc cag ttc aat ctc gtc gga ttc	248
Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn Leu Val Gly Phe	
55 60 65	
atc ttc ttc att acc gcc tcc att ttc gga ttc aca gtt atc ttc atg	296
Ile Phe Phe Ile Thr Ala Ser Ile Phe Gly Phe Thr Val Ile Phe Met	
70 75 80 85	
tcc cga cct aga tcc gtt tac ctc ctc gac tac tca tgt tac ctc ccg	344
Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser Cys Tyr Leu Pro	
90 95 100	
ncg gcg aat ctc aaa gtt agc tac cag aca ttc atg aat cat tct aaa	392
Xaa Ala Asn Leu Lys Val Ser Tyr Gln Thr Phe Met Asn His Ser Lys	
105 110 115	
ctg att gaa gat ttc gac gag tgc tgc ctt gag ttc cag cgg aag atc	440
Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe Gln Arg Lys Ile	
120 125 130	
ctg aag cga tcc ggt ctc ggc gaa gag act tac ctc ccg gaa tct atc	488
Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr Leu Pro Glu Ser Ile	
135 140 145	
cac tgc atc ccg ccg cgt ccg act atg gcg gcg gcg cgt gag gaa tgc	536
His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala Arg Glu Glu Ser	
150 155 160 165	
gag cag gta atc ttc ggt gca ctc gac aat ctc ttc gag aat acc aaa	584
Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe Glu Asn Thr Lys	
170 175 180	
atc gac cct agg gag att ggt gtt gtg gtg gtg aac tgc agc ttg ttt	632
Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn Cys Ser Leu Phe	
185 190 195	
aac ccg acg cct tct tta tcc gcc atg att gtg aac aag tat aag ctt	680
Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu	
200 205 210	
aga gga aac gtg aag agc ttt aac ctc gga gga atg gga tgt agg gct	728
Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Arg Ala	
215 220 225	
ggt gtc atc gcc gtt gat ctc gct aat gac att tta cag ctc cat aga	776
Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile Leu Gln Leu His Arg	
230 235 240 245	

41

aac aca tta gct ctt gtg gtt agc aca gag aac atc act cag aat tgg	824
Asn Thr Leu Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp	
250 255 260	
tac ttt ggt aac aac aaa gca atg ttg att cct aat tgc ttg ttt agg	872
Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg	
265 270 275	
gtt ggt gga tcc gcg gtt ctg ctt tcg aac aag cct cgt gat cga aaa	920
Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys Pro Arg Asp Arg Lys	
280 285 290	
cga tcc aag tat aaa ctt gtt cac acg gta cgg act cat aaa gga tct	968
Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ser	
295 300 305	
gat gag aaa gca ttc aac tgt gtg tac caa gaa caa gac gag gac ttg	1016
Asp Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu Gln Asp Glu Asp Leu	
310 315 320 325	
aaa acc gga gtt tct ttg tct aaa gac cta atg tct ata gct gga gaa	1064
Lys Thr Gly Val Ser Leu Ser Lys Asp Leu Met Ser Ile Ala Gly Glu	
330 335 340	
gct cta aag aca aat atc acc act ttg ggt cct ctg gtt ctt cca ata	1112
Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile	
345 350 355	
agc gag cag att ctg ttc att gcg act ttt gtt gca aag aga ttg ttc	1160
Ser Glu Gln Ile Leu Phe Ile Ala Thr Phe Val Ala Lys Arg Leu Phe	
360 365 370	
agt gcc aag aag aag aag aag aag cct tac ata ccg gat ttc aag ctt	1208
Ser Ala Lys Lys Lys Lys Lys Lys Pro Tyr Ile Pro Asp Phe Lys Leu	
375 380 385	
gcc ttt gat cat ttc tgt att cac gca gga ggt aga gcc gtg atc gat	1256
Ala Phe Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp	
390 395 400 405	
gaa cta gag aag agt tta aag cta ttg cca aaa cat gtg gag gct tct	1304
Glu Leu Glu Lys Ser Leu Lys Leu Leu Pro Lys His Val Glu Ala Ser	
410 415 420	
aga atg aca ttg cat aga ttt gga aac act tca tcg agc tct att tgg	1352
Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp	
425 430 435	
tat gaa tta gct tac aca gaa gct aaa gga aga atg aga aaa ggg aat	1400
Tyr Glu Leu Ala Tyr Thr Glu Ala Lys Gly Arg Met Arg Lys Gly Asn	
440 445 450	

42

cga gtt tgg cag att gct ttt gga agc ggc ttt aag tgt aac agc gcg 1448
 Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala
 455 460 465

gtt tgg gtg gct ctt cgt gat gtc gag ccc tgg gtt aac aat cct tgg 1496
 Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser Val Asn Asn Pro Trp
 470 475 480 485

gaa cat tgc atc cat aga tat ccg gtt aag atc gat ctc tgatttcagc 1545
 Glu His Cys Ile His Arg Tyr Pro Val Lys Ile Asp Leu
 490 495

ttaaccggta aaattgggtct gtacatatat ttaccactga gtaaagacat cagttaatga 1605

tttggtgtta ctcaattggg ctaagtgtat tattatatgt gttgtatata ataaaggtag 1665

aacgtaaatt tactaagaaa aaaaaaaaaa aaaaaaaaaa 1704

<210> 23

<211> 498

<212> PRT

<213> Lunaria annua

<220>

<221> MOD_RES

<222> (102)

<223> Variable amino acid

<400> 23

Met Asp Asp Glu Ser Val Asn Gly Gly Ser Val Gln Ile Arg Thr Arg
 1 5 10 15

Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Ser His Leu Phe Lys
 20 25 30

Leu Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg
 35 40 45

Leu Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe
 50 55 60

Asn Leu Val Gly Phe Ile Phe Phe Ile Thr Ala Ser Ile Phe Gly Phe
 65 70 75 80

Thr Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr
 85 90 95

Ser Cys Tyr Leu Pro Xaa Ala Asn Leu Lys Val Ser Tyr Gln Thr Phe
 100 105 110

Met Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu
 115 120 125

43

Phe Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Glu Thr Tyr
 130 135 140
 Leu Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala
 145 150 155 160
 Ala Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu
 165 170 175
 Phe Glu Asn Thr Lys Ile Asp Pro Arg Glu Ile Gly Val Val Val Val
 180 185 190
 Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val
 195 200 205
 Asn Lys Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly
 210 215 220
 Met Gly Cys Arg Ala Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile
 225 230 235 240
 Leu Gln Leu His Arg Asn Thr Leu Ala Leu Val Val Ser Thr Glu Asn
 245 250 255
 Ile Thr Gln Asn Trp Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro
 260 265 270
 Asn Cys Leu Phe Arg Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys
 275 280 285
 Pro Arg Asp Arg Lys Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg
 290 295 300
 Thr His Lys Gly Ser Asp Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu
 305 310 315 320
 Gln Asp Glu Asp Leu Lys Thr Gly Val Ser Leu Ser Lys Asp Leu Met
 325 330 335
 Ser Ile Ala Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro
 340 345 350
 Leu Val Leu Pro Ile Ser Glu Gln Ile Leu Phe Ile Ala Thr Phe Val
 355 360 365
 Ala Lys Arg Leu Phe Ser Ala Lys Lys Lys Lys Lys Lys Pro Tyr Ile
 370 375 380
 Pro Asp Phe Lys Leu Ala Phe Asp His Phe Cys Ile His Ala Gly Gly
 385 390 395 400
 Arg Ala Val Ile Asp Glu Leu Glu Lys Ser Leu Lys Leu Leu Pro Lys
 405 410 415

44

His Val Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser
 420 425 430

Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Thr Glu Ala Lys Gly Arg
 435 440 445

Met Arg Lys Gly Asn Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe
 450 455 460

Lys Cys Asn Ser Ala Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser
 465 470 475 480

Val Asn Asn Pro Trp Glu His Cys Ile His Arg Tyr Pro Val Lys Ile
 485 490 495

Asp Leu

<210> 24
 <211> 1664
 <212> DNA
 <213> Lunaria annua

<220>
 <221> CDS
 <222> (3)..(1517)

<220>
 <221> modified_base
 <222> (155)
 <223> a, c, t, or g

<220>
 <221> modified_base
 <222> (217)
 <223> a, c, t, or g

<400> 24
 ca atg acg tct gtg aac gta aaa ctc ctt tac cat tac gtc ata acc 47
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr
 1 5 10 15

aac ttt ttc aac ctc tgt ttc ttc cca ctg acg ggg atc ctc gcc gga 95
 Asn Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly
 20 25 30

aaa ggc tct cgt ctt acc aca aac gat ctc cac cac ttc tat tca tat 143
 Lys Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr
 35 40 45

45

ctc caa cac aan ctt ata acc tta acc cta ctc ttt ggc ttc acc gtt	191
Leu Gln His Xaa Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val	
50 55 60	
ttt ggt tgc gtt ctc tac ttc gta anc cga ccc aaa ccg gtt tac ctc	239
Phe Gly Ser Val Leu Tyr Phe Val Xaa Arg Pro Lys Pro Val Tyr Leu	
65 70 75	
gtt gac tac tcc tgc tac ctt cca cca caa cat ctt agc gct ggt atc	287
Val Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile	
80 85 90 95	
tct aag acc atg gaa atc ttt tat caa ata aga aaa tct gat cct tta	335
Ser Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu	
100 105 110	
cga aac gtg gca tta gat gat tgc tct tct ctt gat ttc ttg aga aag	383
Arg Asn Val Ala Leu Asp Asp Ser Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggc gat gaa acc tac ggc ccc gag gga	431
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly	
130 135 140	
ctg ttt gag att cct ccg agg aag aat tta gcg tgc gcg cgt gaa gag	479
Leu Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu	
145 150 155	
acg gag caa gta atc aac ggt gcg cta aaa aat cta ttc gag aac aac	527
Thr Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn	
160 165 170 175	
aaa gtt aac cct aaa gag att ggt ata ctt gtg gtg aac tca agc atg	575
Lys Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat ccg act cct tgc tta tcc gcg atg gta gtt aat act tcc aag	623
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat ctt gga gga atg ggt tgc agt	671
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt atc gcc att gat cta gct aaa gac ttg ttg cat gtt cat	719
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235	
aaa aac aca tat gct ctt gtg gtg agc aca gag aac atc act caa aac	767
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn	
240 245 250 255	

46

att tat acc ggt gat aac aga tcc atg atg gtt tgc aat tgc ttg ttc	815
Ile Tyr Thr Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtc ggt ggg gca gcg att ctg ctc tcc aac aag ccg ggg gat cga	863
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac aag cta gct cac acg gtt cga acg cat acc gga	911
Arg Arg Ser Lys Tyr Lys Leu Ala His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gac aag tct ttt gga tgt gtg cgg caa gaa gaa gat gat agc	959
Ala Asp Asp Lys Ser Phe Gly Cys Val Arg Gln Glu Glu Asp Asp Ser	
305 310 315	
ggt aaa acc gga gtt agt ttg tca aaa gac ata acc gtt gtt gcc ggg	1007
Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Val Val Ala Gly	
320 325 330 335	
ata acg gtt cag aaa aac ata aca aca ttg ggt ccg ttg gtt ctt cct	1055
Ile Thr Val Gln Lys Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro	
340 345 350	
ctg agc gaa aaa atc ctt ttt gtc gtt aca ttc gta gcc aag aaa cta	1103
Leu Ser Glu Lys Ile Leu Phe Val Val Thr Phe Val Ala Lys Lys Leu	
355 360 365	
tta aaa gat aag atc aaa cac tat tac gtg ccg gat ttc aaa ctt gca	1151
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gta gat cat ttc tgt att cat gcg gga ggt aga gcc gtg ata gat gtg	1199
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395	
tta gag aag aac tta ggg cta tgc ccg ata gat gtg gag gca tca aga	1247
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
400 405 410 415	
tca aca tta cat aga ttt ggg aat aca tgc tct agt tca att tgg tat	1295
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag cca aaa gga agg atg aag aaa ggt aat aaa	1343
Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gct tgc caa ata gct ggt ggg tca ggt ttt aag tgt aat agt gcg gtt	1391
Ala Cys Gln Ile Ala Gly Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	

47

tgg gtc gct tta cgc aat gtc gag gct tca gct aat agt cct tgg gaa 1439
 Trp Val Ala Leu Arg Asn Val Glu Ala Ser Ala Asn Ser Pro Trp Glu
 465 470 475

cat tgc att cac aaa tat ccg gtt caa atg tat tct ggt tca tca aag 1487
 His Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys
 480 485 490 495

tca gag act cct gtc caa aac ggt cgg tcc taatttatgt atctcaaatg 1537
 Ser Glu Thr Pro Val Gln Asn Gly Arg Ser
 500 505

atgttggtcca cttctctctt tttttttct ttttttagtt ataatttaat ggttacgatg 1597

ttttgtctag gtcgttataa ataaagaata catgggtggt actagtataa aaaaaaaaaa 1657

aaaaaaaa 1664

<210> 25

<211> 505

<212> PRT

<213> Lunaria annua

<220>

<221> MOD_RES

<222> (51)

<223> Variable amino acid

<220>

<221> MOD_RES

<222> (72)

<223> Variable amino acid

<400> 25

Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15

Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly Lys
 20 25 30

Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr Leu
 35 40 45

Gln His Xaa Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val Phe
 50 55 60

Gly Ser Val Leu Tyr Phe Val Xaa Arg Pro Lys Pro Val Tyr Leu Val
 65 70 75 80

Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile Ser
 85 90 95

48

Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu Arg
 100 105 110
 Asn Val Ala Leu Asp Asp Ser Ser Ser Leu Asp Phe Leu Arg Lys Ile
 115 120 125
 Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly Leu
 130 135 140
 Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu Thr
 145 150 155 160
 Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn Lys
 165 170 175
 Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
 180 185 190
 Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys Leu
 195 200 205
 Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
 210 215 220
 Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
 225 230 235 240
 Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Ile
 245 250 255
 Tyr Thr Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
 260 265 270
 Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
 275 280 285
 Arg Ser Lys Tyr Lys Leu Ala His Thr Val Arg Thr His Thr Gly Ala
 290 295 300
 Asp Asp Lys Ser Phe Gly Cys Val Arg Gln Glu Glu Asp Asp Ser Gly
 305 310 315 320
 Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Val Val Ala Gly Ile
 325 330 335
 Thr Val Gln Lys Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Leu
 340 345 350
 Ser Glu Lys Ile Leu Phe Val Val Thr Phe Val Ala Lys Lys Leu Leu
 355 360 365
 Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Val
 370 375 380

49

Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
385 390 395 400

Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg Ser
405 410 415

Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
420 425 430

Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys Ala
435 440 445

Cys Gln Ile Ala Gly Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
450 455 460

Val Ala Leu Arg Asn Val Glu Ala Ser Ala Asn Ser Pro Trp Glu His
465 470 475 480

Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys Ser
485 490 495

Glu Thr Pro Val Gln Asn Gly Arg Ser
500 505

<210> 26

<211> 1732

<212> DNA

<213> Lunaria annua

<220>

<221> CDS

<222> (19)..(1611)

<400> 26

ctttcttctt ccccaaca atg acc cat aac caa aac caa cct cac cgg gca 51
Met Thr His Asn Gln Asn Gln Pro His Arg Ala
1 5 10

gtt ccg gtt cac gtt aca aac tcc gat caa aac caa aac caa aac caa 99
Val Pro Val His Val Thr Asn Ser Asp Gln Asn Gln Asn Gln Asn Gln
15 20 25

aac aat ctc cca aat ttt ctc tta tct gtt cgg ctc aaa tat gta aaa 147
Asn Asn Leu Pro Asn Phe Leu Leu Ser Val Arg Leu Lys Tyr Val Lys
30 35 40

ctt ggg tac cat tac cta atc tcc aac ggt ctc tac atc ctc ctc ctc 195
Leu Gly Tyr His Tyr Leu Ile Ser Asn Gly Leu Tyr Ile Leu Leu Leu
45 50 55

50

cct ctc ctc ggc ggc aca atc gta aaa ctc tct tcc ttc aca ctc aac Pro Leu Leu Gly Gly Thr Ile Val Lys Leu Ser Ser Phe Thr Leu Asn 60 65 70 75	243
gaa ctc tct ctc ctc tac aac cac ctc cgt ttt cat ttc ctc tcc gcc Glu Leu Ser Leu Leu Tyr Asn His Leu Arg Phe His Phe Leu Ser Ala 80 85 90	291
aca ctc gct acc gga ctc tta atc tct ctc tcc acc gcc tac ttc acc Thr Leu Ala Thr Gly Leu Leu Ile Ser Leu Ser Thr Ala Tyr Phe Thr 95 100 105	339
acc cgt cct cgt cat gtc ttc ctc ctc gac ttc tca tgc tac aaa cct Thr Arg Pro Arg His Val Phe Leu Asp Phe Ser Cys Tyr Lys Pro 110 115 120	387
gac cct tcc tta ata tgc act cgt gaa aca ttc atg gac cga tct caa Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp Arg Ser Gln 125 130 135	435
cgt gta ggt atc ttc aca gaa gac aac ctc gct ttt caa caa aag atc Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln Gln Lys Ile 140 145 150 155	483
ctc gaa aga tcc ggt ctt ggg cag aaa act tac ttc cct gaa gct ctt Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro Glu Ala Leu 160 165 170	531
ctt cgt gtt cct ccc aat cct tgt atg gaa gaa gcg aga aaa gaa gca Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg Lys Glu Ala 175 180 185	579
gag act gtt atg ttc gga gct ata gac tct gtt ctt gag aaa acc ggt Glu Thr Val Met Phe Gly Ala Ile Asp Ser Val Leu Glu Lys Thr Gly 190 195 200	627
gtg aaa cct aaa gat atc gga atc ctt gtc gtg aat tgt agt ttg ttt Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe 205 210 215	675
aat ccg acg ccg tca ctt tcc gcc atg att gtg aat aag tat aag ctt Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu 220 225 230 235	723
aga gga aac att ttg agc tat aat ctc ggt gga atg ggt tgt agt gct Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala 240 245 250	771
gga ctt atc tcc att gat ctc gct aaa cag ctt ctt cag gtc caa cca Gly Leu Ile Ser Ile Asp Leu Ala Lys Gln Leu Leu Gln Val Gln Pro 255 260 265	819

51

aac tca tac gca cta gtg gtg agc aca gag aac ata acc tta aac tgg Asn Ser Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp 270 275 280	867
tac tta ggc aac gac cga tca atg ctt ctc tct aac tgc atc ttc cgt Tyr Leu Gly Asn Asp Arg Ser Met Leu Leu Ser Asn Cys Ile Phe Arg 285 290 295	915
atg gga gga gcc gcc gta ctt ctc tca aac cgt tcc tcc gat cgc acc Met Gly Gly Ala Ala Val Leu Leu Ser Asn Arg Ser Ser Asp Arg Thr 300 305 310 315	963
cgt tca aaa tat cag ctc atc cac ccc gtc cgt acc cac aaa gga gcc Arg Ser Lys Tyr Gln Leu Ile His Pro Val Arg Thr His Lys Gly Ala 320 325 330	1011
aac gac aac gca ttt ggc tgc gtt tac caa cga gaa gac aac aac gaa Asn Asp Asn Ala Phe Gly Cys Val Tyr Gln Arg Glu Asp Asn Asn Glu 335 340 345	1059
gaa gaa acc gcc aaa atc gga gtc tca ctc tct aaa aac cta atg gca Glu Glu Thr Ala Lys Ile Gly Val Ser Leu Ser Lys Asn Leu Met Ala 350 355 360	1107
ata gcc gga gaa gct ctc aag aca aac ata aca aca ctc gga cca cta Ile Ala Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu 365 370 375	1155
gtc tta cca atg tcc gaa cag att ctg ttt ttc cca aca ctc gtg gct Val Leu Pro Met Ser Glu Gln Ile Leu Phe Phe Pro Thr Leu Val Ala 380 385 390 395	1203
cga aaa atc ttc aaa gtc aag aaa ata aag cct tac ata ccc gat ttc Arg Lys Ile Phe Lys Val Lys Lys Ile Lys Pro Tyr Ile Pro Asp Phe 400 405 410	1251
aag cta gct ttc gag cat ttc tgc atc cat gcg gga ggt aga gca gtg Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala Val 415 420 425	1299
ctt gat gag ata gag aag aat ttg gat tta tca gag tgg cat atg gaa Leu Asp Glu Ile Glu Lys Asn Leu Asp Leu Ser Glu Trp His Met Glu 430 435 440	1347
cca tcg agg atg act tta aac cgg ttt ggt aat act tcg agt agc tca Pro Ser Arg Met Thr Leu Asn Arg Phe Gly Asn Thr Ser Ser Ser Ser 445 450 455	1395
ctt tgg tat gaa ctt gcg tat agt gaa gct aaa ggg agg att aag aga Leu Trp Tyr Glu Leu Ala Tyr Ser Glu Ala Lys Gly Arg Ile Lys Arg 460 465 470 475	1443

52

gga gat agg act tgc caa att gcg ttt gga tcg gga ttt aag tgt aat 1491
 Gly Asp Arg Thr Cys Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn
 480 485 490

agt gcg gtt tgg aaa gct ttg aga acc att gat cct att gat gag aag 1539
 Ser Ala Val Trp Lys Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys
 495 500 505

aag aat cca tgg agt gat gag att cat gag ttt cca gtt tct gtt cct 1587
 Lys Asn Pro Trp Ser Asp Glu Ile His Glu Phe Pro Val Ser Val Pro
 510 515 520

agg atc act cca gtt act tct aac tagtggtttt tttttgggtc caactagggg 1641
 Arg Ile Thr Pro Val Thr Ser Asn
 525 530

caatatttgt tatggttttg ttcttacgta cgtactttaa gtgatttagt ctaaaaataa 1701

attggtttca taaaaaaaaa aaaaaaaaaa a 1732

<210> 27

<211> 531

<212> PRT

<213> Lunaria annua

<400> 27

Met Thr His Asn Gln Asn Gln Pro His Arg Ala Val Pro Val His Val
 1 5 10 15

Thr Asn Ser Asp Gln Asn Gln Asn Gln Asn Gln Asn Asn Leu Pro Asn
 20 25 30

Phe Leu Leu Ser Val Arg Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr
 35 40 45

Leu Ile Ser Asn Gly Leu Tyr Ile Leu Leu Leu Pro Leu Leu Gly Gly
 50 55 60

Thr Ile Val Lys Leu Ser Ser Phe Thr Leu Asn Glu Leu Ser Leu Leu
 65 70 75 80

Tyr Asn His Leu Arg Phe His Phe Leu Ser Ala Thr Leu Ala Thr Gly
 85 90 95

Leu Leu Ile Ser Leu Ser Thr Ala Tyr Phe Thr Thr Arg Pro Arg His
 100 105 110

Val Phe Leu Leu Asp Phe Ser Cys Tyr Lys Pro Asp Pro Ser Leu Ile
 115 120 125

Cys Thr Arg Glu Thr Phe Met Asp Arg Ser Gln Arg Val Gly Ile Phe
 130 135 140

53

Thr Glu Asp Asn Leu Ala Phe Gln Gln Lys Ile Leu Glu Arg Ser Gly
 145 150 155 160
 Leu Gly Gln Lys Thr Tyr Phe Pro Glu Ala Leu Leu Arg Val Pro Pro
 165 170 175
 Asn Pro Cys Met Glu Glu Ala Arg Lys Glu Ala Glu Thr Val Met Phe
 180 185 190
 Gly Ala Ile Asp Ser Val Leu Glu Lys Thr Gly Val Lys Pro Lys Asp
 195 200 205
 Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser
 210 215 220
 Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly Asn Ile Leu
 225 230 235 240
 Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile
 245 250 255
 Asp Leu Ala Lys Gln Leu Leu Gln Val Gln Pro Asn Ser Tyr Ala Leu
 260 265 270
 Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Leu Gly Asn Asp
 275 280 285
 Arg Ser Met Leu Leu Ser Asn Cys Ile Phe Arg Met Gly Gly Ala Ala
 290 295 300
 Val Leu Leu Ser Asn Arg Ser Ser Asp Arg Thr Arg Ser Lys Tyr Gln
 305 310 315 320
 Leu Ile His Pro Val Arg Thr His Lys Gly Ala Asn Asp Asn Ala Phe
 325 330 335
 Gly Cys Val Tyr Gln Arg Glu Asp Asn Asn Glu Glu Glu Thr Ala Lys
 340 345 350
 Ile Gly Val Ser Leu Ser Lys Asn Leu Met Ala Ile Ala Gly Glu Ala
 355 360 365
 Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser
 370 375 380
 Glu Gln Ile Leu Phe Phe Pro Thr Leu Val Ala Arg Lys Ile Phe Lys
 385 390 395 400
 Val Lys Lys Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu
 405 410 415
 His Phe Cys Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Ile Glu
 420 425 430

54

Lys Asn Leu Asp Leu Ser Glu Trp His Met Glu Pro Ser Arg Met Thr
435 440 445

Leu Asn Arg Phe Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu
450 455 460

Ala Tyr Ser Glu Ala Lys Gly Arg Ile Lys Arg Gly Asp Arg Thr Cys
465 470 475 480

Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys
485 490 495

Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys Lys Asn Pro Trp Ser
500 505 510

Asp Glu Ile His Glu Phe Pro Val Ser Val Pro Arg Ile Thr Pro Val
515 520 525

Thr Ser Asn
530

<210> 28

<211> 622

<212> DNA

<213> Tropaeolum majus

<220>

<221> CDS

<222> (1)..(621)

<400> 28

aag ctt aaa cta gta tac cat tac ttg atc tcc aac gcc atg tat ttg 48
Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu
1 5 10 15

tta atg gtg ccg ctt cta gca gta gcc ttt gct cat ctc tcc acg ttg 96
Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu
20 25 30

acg att caa gat ctg gtt cat ctt tgg gaa cag ctt aag ttc aat tta 144
Thr Ile Gln Asp Leu Val His Leu Trp Glu Gln Leu Lys Phe Asn Leu
35 40 45

ctg tca gta act ctc tgc tgc agc ctt atg gtg ttt tta ggg act ctg 192
Leu Ser Val Thr Leu Cys Ser Ser Leu Met Val Phe Leu Gly Thr Leu
50 55 60

tat ttc atg agc cga ccg acg aag att tac ttg gtg gat ttc tct tgt 240
Tyr Phe Met Ser Arg Pro Thr Lys Ile Tyr Leu Val Asp Phe Ser Cys
65 70 75 80

55

tac aag ccg gaa aaa gag cgt ata tgc acg aga gag att ttc tat gag 288
 Tyr Lys Pro Glu Lys Glu Arg Ile Cys Thr Arg Glu Ile Phe Tyr Glu
 85 90 95

aga tcg aaa cta act ggg aat ttt acc gat gat aat tta act ttc caa 336
 Arg Ser Lys Leu Thr Gly Asn Phe Thr Asp Asp Asn Leu Thr Phe Gln
 100 105 110

aag aaa att atc gaa aga tct gga tta ggt cag aac acg tac tta cct 384
 Lys Lys Ile Ile Glu Arg Ser Gly Leu Gly Gln Asn Thr Tyr Leu Pro
 115 120 125

gag gcc gtt cta cgg gtt ccg ccc aat ccg tgt atg gcg gag gct aga 432
 Glu Ala Val Leu Arg Val Pro Pro Asn Pro Cys Met Ala Glu Ala Arg
 130 135 140

aag gag gct gag atg gtt atg ttc ggt gcg atc gat gaa ttg ttg gag 480
 Lys Glu Ala Glu Met Val Met Phe Gly Ala Ile Asp Glu Leu Leu Glu
 145 150 155 160

aaa acc ggg gtt aaa cct aag gat atc ggt att ctt gtg gtg aat tgc 528
 Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
 165 170 175

agc ttg ttc aat ccg acg ccg tct ctg tcc gca atg gtg gtt aat cgg 576
 Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Arg
 180 185 190

tac aag ctt aga ggg aat atc ata agt tat aac ctt ggc ggg atg g 622
 Tyr Lys Leu Arg Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met
 195 200 205

<210> 29

<211> 207

<212> PRT

<213> Tropaeolum majus

<400> 29

Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu
 1 5 10 15

Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu
 20 25 30

Thr Ile Gln Asp Leu Val His Leu Trp Glu Gln Leu Lys Phe Asn Leu
 35 40 45

Leu Ser Val Thr Leu Cys Ser Ser Leu Met Val Phe Leu Gly Thr Leu
 50 55 60

Tyr Phe Met Ser Arg Pro Thr Lys Ile Tyr Leu Val Asp Phe Ser Cys
 65 70 75 80

56

Tyr Lys Pro Glu Lys Glu Arg Ile Cys Thr Arg Glu Ile Phe Tyr Glu
85 90 95

Arg Ser Lys Leu Thr Gly Asn Phe Thr Asp Asp Asn Leu Thr Phe Gln
100 105 110

Lys Lys Ile Ile Glu Arg Ser Gly Leu Gly Gln Asn Thr Tyr Leu Pro
115 120 125

Glu Ala Val Leu Arg Val Pro Pro Asn Pro Cys Met Ala Glu Ala Arg
130 135 140

Lys Glu Ala Glu Met Val Met Phe Gly Ala Ile Asp Glu Leu Leu Glu
145 150 155 160

Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
165 170 175

Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Arg
180 185 190

Tyr Lys Leu Arg Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met
195 200 205

<210> 30

<211> 11

<212> PRT

<213> Simmondsia chinensis

<400> 30

Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Lys
1 5 10

<210> 31

<211> 10

<212> PRT

<213> Simmondsia chinensis

<220>

<221> MOD_RES

<222> (3)

<223> Unknown

<220>

<221> MOD_RES

<222> (10)

<223> Unknown

<400> 31

Val Pro Xaa Glu Pro Ser Ile Ala Ala Xaa
1 5 10

57

<210> 32
<211> 10
<212> PRT
<213> *Simmondsia chinensis*

<400> 32
Glu Thr Tyr Val Pro Glu Glu Val Thr Lys
1 5 10

<210> 33
<211> 11
<212> PRT
<213> *Simmondsia chinensis*

<400> 33
Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys
1 5 10

<210> 34
<211> 11
<212> PRT
<213> *Simmondsia chinensis*

<400> 34
Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe
1 5 10

<210> 35
<211> 11
<212> PRT
<213> *Simmondsia chinensis*

<220>
<221> MOD_RES
<222> (4)..(5)
<223> Unknown

<400> 35
Phe Leu Pro Xaa Xaa Val Ala Ile Thr Gly Glu
1 5 10

<210> 36
<211> 17
<212> PRT
<213> *Simmondsia chinensis*

58

<220>
<221> MOD_RES
<222> (7)..(8)
<223> Unknown

<220>
<221> MOD_RES
<222> (11)
<223> Unknown

<400> 36
Phe Gly Asn Thr Ser Ser Xaa Xaa Leu Tyr Xaa Glu Leu Ala Tyr Ala
1 5 10 15

Lys

<210> 37
<211> 17
<212> PRT
<213> *Simmondsia chinensis*

<400> 37
Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu
1 5 10 15

Lys

<210> 38
<211> 23
<212> PRT
<213> *Acinetobacter* sp.

<220>
<221> MOD_RES
<222> (1)
<223> Unknown

<220>
<221> MOD_RES
<222> (17)
<223> Unknown

<400> 38
Xaa Asp Ile Ala Ile Ile Gly Ser Gly Ser Ala Gly Leu Ala Gln Ala
1 5 10 15

Xaa Ile Leu Lys Asp Ala Gly
20

59

<210> 39
<211> 13
<212> PRT
<213> *Acinetobacter* sp.

<220>
<221> MOD_RES
<222> (7)
<223> Unknown

<400> 39
Gln Gln Phe Thr Val Trp Xaa Asn Ala Ser Glu Pro Ser
1 5 10

<210> 40
<211> 6
<212> PRT
<213> *Simmondsia chinensis*

<400> 40
Asn Ile Thr Thr Leu Gly
1 5

<210> 41
<211> 6
<212> PRT
<213> *Simmondsia chinensis*

<400> 41
Ser Asn Cys Lys Phe Gly
1 5

<210> 42
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (9)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (12)
<223> a, c, t, g, other or unknown

60

<220>
<221> modified_base
<222> (15)
<223> a, c, t, g, other or unknown

<400> 42
aayathacna cnytnngg

17

<210> 43
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (15)
<223> a, c, t, g, other or unknown

<400> 43
swrttrcayt traancc

17

<210> 44
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA Molecule:
Synthetic primer

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 44
caucaucauc augtcgacaa aatgacgtcc attaacgtaa ag

42

<210> 45
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA Molecule:
Synthetic primer

61

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 45

cuacuacuac uagtcgacgg atcctatttg gaagctttga cattgttttag

50

<210> 46

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (3)

<223> Leu or Gly

<400> 46

Lys Leu Xaa Tyr His Tyr

1

5

<210> 47

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Combined DNA/RNA Molecule:
Synthetic primer

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<220>

<221> modified_base

<222> (30)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (33)

<223> a, c, t, g, other or unknown

<400> 47

caucaucauc augaattcaa gcttaarytn bkntaycayt a

41

62

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 48
Asn Leu Gly Gly Met Gly Cys
1 5

<210> 49
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA Molecule:
Synthetic primer

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (30)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (33)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (36)
<223> a, c, t, g, other or unknown

<400> 49
caucaucauc augaattcaa gcttaayytn ggnngnatgg g

41

<210> 50
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA Molecule:
Synthetic primer

63

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (29)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (32)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (35)
<223> a, c, t, g, other or unknown

<400> 50
cuacuacuac uaggatccgt cgacccatnc cnccnarrtt

40

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 51
Gly Phe Lys Cys Asn Ser
1 5

<210> 52
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA Molecule:
Synthetic primer

<220>
<223> Description of Artificial Sequence: Synthetic
primer

64

<220>

<221> modified_base

<222> (39)

<223> a, c, t, g, other or unknown

<400> 52

cuacuacuac uaggatccgt cgacswrttr cayttraanc c

41

<210> 53

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Combined DNA/RNA Molecule:
Synthetic primer

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<220>

<221> modified_base

<222> (27)

<223> a, c, t, g, other or unknown

<400> 53

cuacuacuac uaswrttrca yttraancc

29